

# BLAST Basic Local Alignment Search Tool

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Blast 2 sequences

## J01749:Cloning vector pBR322, complete sequence

Results for: gb|J01749.1 Cloning vector pBR322, complete sequence(4361bp)

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

gi|208958|gb|J01749.1|SYNPBR322

Description

Cloning vector pBR322, complete sequence

Molecule type

nucleic acid

Query Length

4361

Subject ID

gi|335823|gb|J02425.1|VACTKN

Description

vaccinia virus thymidine kinase gene and flanks

Molecule type

nucleic acid

Subject Length

794

Program

BLASTN 2.2.19+ [Citation](#)

## Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402.

Other reports: [Search Summary](#) [[Taxonomy reports](#)]

## Search Parameters

Program	blastn
Word size	7
Expect value	10
Hittlist size	100
Match/Mismatch scores	2,-3
Gapcosts	5,2
Filter string	F
Genetic Code	1

## Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408146	0.41
H	0.912438	0.78

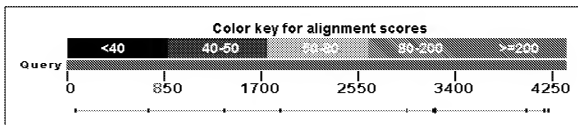
## Results Statistics

[Graphic Summary](#)

## Distribution of 10 Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.



## Plot of gi|208958|gb|J01749.1|SYNPBR322 vs gi|335823|gb|J02425.1|VACTKN [?]

This dot matrix view shows regions of similarity based upon the BLAST results. The query sequence is represented on the X-axis and the numbers represent the bases/residues of the query. The subject is represented on the Y-axis and again the numbers represent the bases/residues of the subject. Alignments are shown in the plot as lines. Plus strand and protein matches are slanted from the bottom left to the upper right corner, minus strand matches are slanted from the upper left to the lower right. The number of lines shown in the plot is the same as the number of alignments found by BLAST.



## Descriptions

Legend for links to other resources: UniGene GEO Gene Structure Map Viewer

## Sequences producing significant alignments:

(Click headers to sort columns)

22.9	200	3%	0.42	100%
J02425.1	vaccinia virus thymidine kinase gene and flanks			

Alignments **Select All** Get selected sequences Distance tree of results

>gb|J02425.1|VACTKN vaccinia virus thymidine kinase gene and flanks  
Length=794

Sort alignments for this subject sequ  
E value Score Percent identity  
Query start position Subject start

Score = 22.9 bits (24), Expect = 0.42  
Identities = 15/17 (88%), Gaps = 0/17 (0%)  
Strand=Plus/Plus

Query 4168 AATATTATTGAAGCATT 4184  
|||||  
Sbjct 390 AATAATTTTGAAGCATT 406

Score = 21.1 bits (22), Expect = 1.5  
Identities = 14/16 (87%), Gaps = 0/16 (0%)  
Strand=Plus/Minus

Query 1378 AACATATCCATCGCGT 1393  
|||  
Sbjct 181 AATATATCCATCACGT 166

Score = 21.1 bits (22), Expect = 1.5  
Identities = 11/11 (100%), Gaps = 0/11 (0%)  
Strand=Plus/Plus

Query 82 GTGTATGAAAT 92  
|||||  
Sbjct 635 GTGTATGAAAT 645

Score = 19.3 bits (20), Expect = 5.2  
Identities = 16/20 (80%), Gaps = 0/20 (0%)  
Strand=Plus/Minus

Query 4205 GAGCGGATACATATTTGAAT 4224  
||| |||  
Sbjct 102 GAGAGGATTCITTTTGAAT 83

Score = 19.3 bits (20), Expect = 5.2  
Identities = 13/15 (86%), Gaps = 0/15 (0%)  
Strand=Plus/Plus

Query 3222 TAGATCCTTTTAAAT 3236  
|||||  
Sbjct 118 TAGATCCTGTTAGAT 132

Score = 19.3 bits (20), Expect = 5.2  
Identities = 13/15 (86%), Gaps = 0/15 (0%)  
Strand=Plus/Minus

Query 3202 TATCAAAAAGGATCT 3216  
|||||  
Sbjct 133 TATCTAACAGGATCT 119

Score = 19.3 bits (20), Expect = 5.2  
Identities = 10/10 (100%), Gaps = 0/10 (0%)

Strand=Plus/Plus

Query 2971 GAAGGACAGT 2980  
          |||||  
Sbjct 471 GAAGGACAGT 480

Score = 19.3 bits (20), Expect = 5.2  
Identities = 13/15 (86%), Gaps = 0/15 (0%)  
Strand=Plus/Plus

Query 715 TATCGTCGCCGCACT 729  
          ||| || |||  
Sbjct 536 TATAGTAGCCGCACT 550

Score = 19.3 bits (20), Expect = 5.2  
Identities = 12/13 (92%), Gaps = 0/13 (0%)  
Strand=Plus/Minus

Query 1869 TATCATTACCCCC 1881  
          |||||  
Sbjct 717 TATCATTACCTCC 705

Score = 19.3 bits (20), Expect = 5.2  
Identities = 10/10 (100%), Gaps = 0/10 (0%)  
Strand=Plus/Minus

Query 4017 TCGATGTAAC 4026  
          |||||  
Sbjct 751 TCGATGTAAC 742

Select All Get selected sequences Distance tree of results